e_val_multi_group_model

April 28, 2020

0.1 Eigenvalue Change of Next Generation Matrix

Analytically derived a formula to predict the change in the largest eigenvalue of the next generation matrix when we remove one type of infected individual from a multi-group SIR model. This has importance as the largest eigenvalue/spectral radius of the next generation matrix gives the R_0 for the system.

If we consider $\mathbf{G}$ to be the next generation matrix for the entire multigroup model, with largest eigenvalue λ that has associated left and right eigenvectors $\mathbf{v}^T$ and $\mathbf{u}$, then we define the relative importance of an infective node I_k to be

$$\mathcal{I}_k = -\frac{\Delta\lambda}{\lambda}$$

where $\Delta\lambda$ is the change in the largest eigenvalue upon removal of I_k from the system. We derived the following analytical approximation

$$\mathcal{I}_k = \frac{\mathbf{u}_k\mathbf{v}_k}{\mathbf{v}^T\mathbf{u} - \mathbf{u}_k\mathbf{v}_k}.$$

In this notebook, we will apply this approximation to a self-generated toy example.

0.1.1 The Model

Each state has an average transmission rate $B_i = \sum_{j=1}^{7} B_{j,i}$ which gives a rate at which state i infects the other states (including itself). We consider the following multi-group model:

$$\frac{dS_i}{dt} = -\sum_{j=0}^{7} B_{i,j} N_i I_j \tag{1}$$

$$\frac{dI_i}{dt} = \sum_{j=0}^{7} B_{i,j} S_i I_j - \gamma_i I_i \tag{2}$$

$$\frac{dR_i}{dt} = \gamma_i I_i \tag{3}$$

.

This system has a disease free solution, when $I_j = 0\,\forall\, i$, and $S_i^* = \frac{\Lambda_i}{\mu_i}$.

0.1.2 Age Groups

Group data using pre-specified groups from PLOS data.

In [114]:
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd

matplotlib.rc('text', usetex=True)
matplotlib.rcParams['text.latex.preamble']=[r"\usepackage{amsmath}"]
```

Importing Data from Contact Rate Paper Paper Reference: https://journals.plos.org/plosmedicine/article?id=10.1371/journal.pmed.0050074#s5 We specifically use data from the Table S8.4b), which we have converted into csv format.

In [557]:
```
full_data = pd.read_csv("data/contact_data.csv", index_col=0)
full_data
```

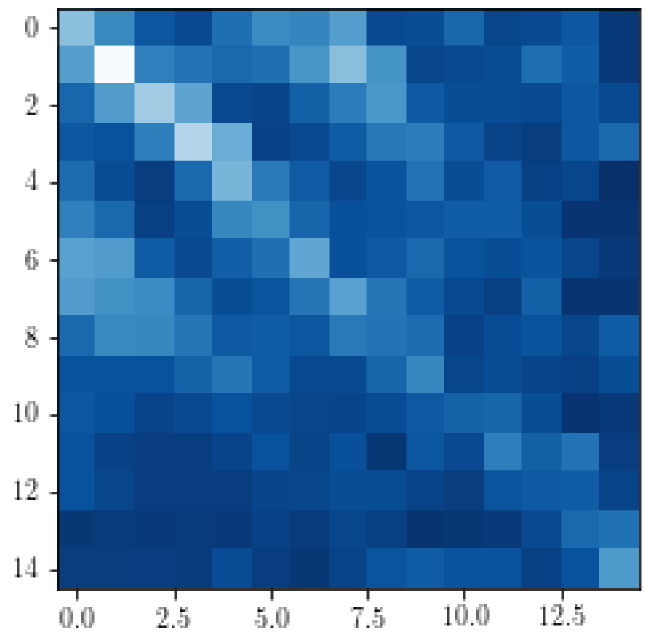
Out[557]:
```
       2     7    12    17    22    27    32    37    42    47    52    57  \
2   1.00  0.59  0.25  0.18  0.42  0.61  0.57  0.74  0.18  0.20  0.36  0.15
7   0.74  1.72  0.53  0.44  0.37  0.42  0.68  0.99  0.66  0.15  0.17  0.19
12  0.36  0.73  1.09  0.79  0.17  0.14  0.32  0.51  0.69  0.27  0.20  0.19
17  0.26  0.22  0.52  1.20  0.85  0.12  0.17  0.29  0.48  0.51  0.27  0.13
22  0.39  0.19  0.09  0.38  0.92  0.49  0.28  0.16  0.23  0.44  0.20  0.28
27  0.53  0.37  0.11  0.20  0.58  0.64  0.35  0.21  0.23  0.25  0.30  0.30
32  0.77  0.72  0.29  0.17  0.31  0.42  0.80  0.21  0.27  0.38  0.23  0.20
37  0.73  0.65  0.61  0.35  0.20  0.24  0.47  0.76  0.47  0.29  0.18  0.11
42  0.38  0.59  0.58  0.47  0.27  0.29  0.25  0.49  0.45  0.40  0.12  0.19
47  0.22  0.23  0.22  0.34  0.46  0.29  0.17  0.17  0.35  0.58  0.15  0.19
52  0.26  0.21  0.14  0.17  0.22  0.17  0.15  0.14  0.19  0.27  0.33  0.35
57  0.22  0.12  0.10  0.10  0.14  0.22  0.13  0.21  0.05  0.25  0.17  0.52
62  0.22  0.15  0.10  0.10  0.10  0.14  0.15  0.20  0.19  0.13  0.09  0.24
67  0.05  0.08  0.07  0.08  0.07  0.12  0.08  0.16  0.11  0.04  0.05  0.07
72  0.09  0.09  0.10  0.08  0.19  0.10  0.05  0.13  0.24  0.29  0.23  0.22

      62    67    72
2   0.18  0.26  0.07
7   0.41  0.30  0.07
12  0.17  0.26  0.17
17  0.09  0.26  0.37
22  0.11  0.15  0.00
27  0.20  0.04  0.03
32  0.23  0.15  0.07
37  0.32  0.04  0.03
42  0.23  0.15  0.30
47  0.14  0.11  0.20
52  0.20  0.04  0.07
57  0.32  0.44  0.10
62  0.27  0.30  0.13
```

```
67  0.17  0.37  0.43
72  0.11  0.22  0.70
```

```
In [558]: age_range = [2,7,12,17,22,27,32,37,42,47, 52,57,62,67,"70+"]
```

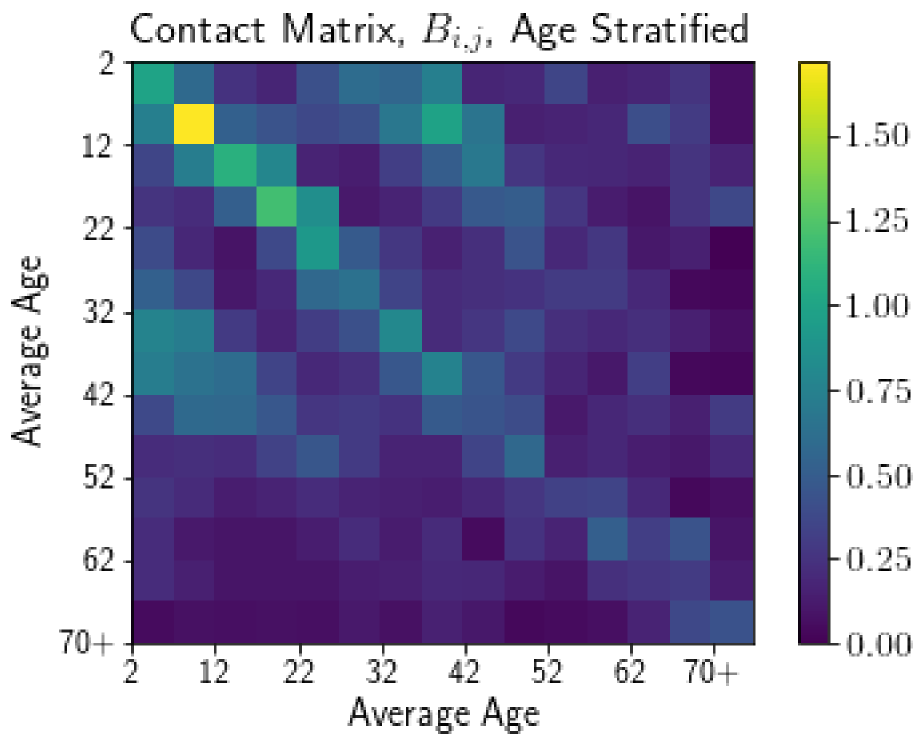
```
In [559]: full_data = full_data.values
          plt.imshow(full_data, cmap = "Blues_r")
```

```
Out[559]: <matplotlib.image.AxesImage at 0x140c414e9b0>
```




```
In [560]: plt.imshow(full_data, interpolation="nearest")
          x = np.arange(0,15,1) # the grid to which your data corresponds
          nx = x.shape[0]
          no_labels = 7 # how many labels to see on axis x
          step_x = int(nx / (no_labels - 1)) # step between consecutive labels
          x_positions = np.arange(-0.5,nx - 0.5,step_x) # pixel count at label position
          x_labels = x[::step_x] # labels you want to see

          final_labels = []
          for idx in x_labels.astype(int):
              if idx == 15:
                  final_labels.append(age_range[idx - 1])
              else:
                  final_labels.append(age_range[idx])
          plt.xticks(x_positions, final_labels)
          plt.yticks(x_positions, final_labels)
```

```
plt.xlabel("Average Age", fontsize = 14)
plt.ylabel("Average Age", fontsize = 14)
plt.title("Contact Matrix, $B_{i,j}$, Age Stratified", fontsize = 16)
plt.xticks(fontsize=12, rotation=0)
plt.yticks(fontsize=12, rotation=0)
cbar = plt.colorbar()
cbar.ax.tick_params(labelsize=14)

#plt.savefig("imgs/contract_rate_matrix.pdf", bbox_inches = "tight")
```




```
In [493]: data = full_data
```

```
In [536]: # aggregate to less granular level -  not used

          # tempdata = np.zeros((5,15))

          # #bins = [12, 27, 42, 57, 72]
          # bins = [2, 5, 8, 11, 14]
          # count = 0
          # for i in bins:
          #     tempdata[count, :] = np.mean((full_data[i], full_data[i - 1], full_data[i -2]
          #     count+=1
```

```
# tempdata

# contact_data = np.zeros((5,5))

# cols = [2, 5, 8, 11, 14]
# count = 0

# for row in range(len(tempdata)):
#     count  = 0
#     for col in cols:
#         contact_data[row, count] = np.mean((tempdata[row, col], tempdata[row, col
#         count+=1


# plt.imshow(contact_data, cmap = "Blues_r")
```

0.2 Defining other model parameters

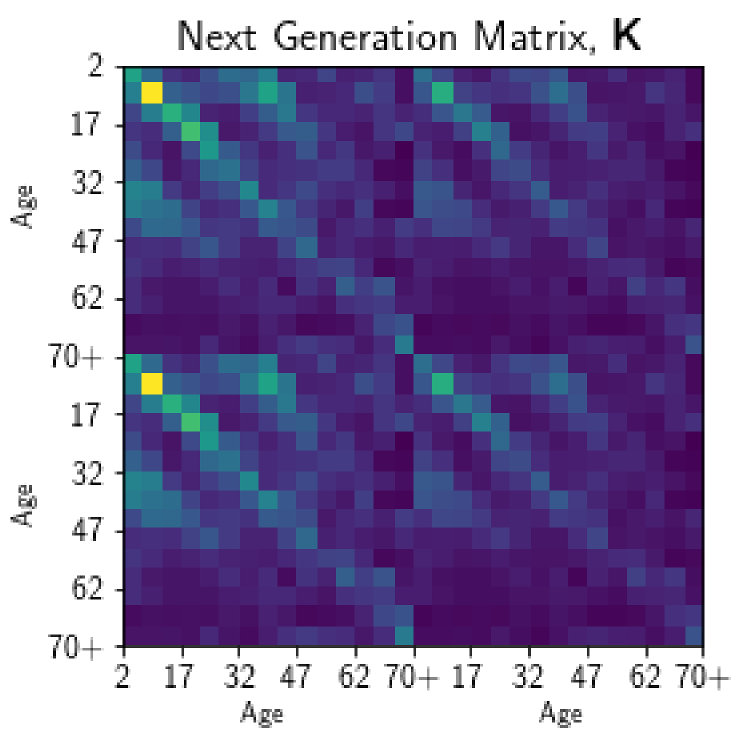
We need to define the following for the model: - The recovery rates of the fast and slow reporters. - The population of each type (we assume the same population level for each type, which appears to be realistic, https://www.statista.com/statistics/281174/uk-population-by-age/)

```
In [542]: # Slow reporters (gamma_1)

          gamma_1 = 0.5

          # Fast Reporters (gamma_2)

          gamma_2 = 0.8

          gamma = [gamma_1]*len(data) + [gamma_2]*len(data) # recovery rates for the 10 differ
```

```
In [543]: # generating the next generation matrix K

          K = np.zeros((len(data)*2,len(data)*2))

          for i in range(len(K)):
              for j in range(len(K)):
                  K[i,j] = data[i % len(data),j % len(data)] / gamma[j]
```

```
In [561]: plt.imshow(K, interpolation="none", extent=[0,30,30,0])
          plt.title("Next Generation Matrix, $\\textbf{K}$", fontsize = 16)


          x = np.arange(0,31,1) # the grid to which your data corresponds
          nx = x.shape[0]
          no_labels = 10 # how many labels to see on axis x
          step_x = int(nx / (no_labels - 1)) # step between consecutive labels
          x_positions = np.arange(0,nx,step_x) # pixel count at label position
```

```
x_labels = x[::step_x] # labels you want to see
x_labels = x_labels % 15
x_labels[5] = 15
x_labels[10] = 15

final_labels = []
for idk in x_labels:
    if idk == 15:
        final_labels.append(age_range[idk -1])
    else:
        final_labels.append(age_range[idk])

plt.xticks(x_positions, final_labels, fontsize = 12)
plt.yticks(x_positions, final_labels, fontsize = 12)
plt.ylabel("Age $\qquad \qquad \qquad  \qquad \quad$ Age")
plt.xlabel("Age $\qquad \qquad \qquad  \qquad \quad$ Age")

#plt.savefig("imgs/next_gen_matrix.png", dpi = 600, bbox_inches = "tight")
```



0.2.1 Finding the $\mathcal{R}_0$ of the model and eigenvalue decomposition.

```
In [545]: import scipy.linalg

          values, left, right = scipy.linalg.eig(K, right = True, left = True)
```

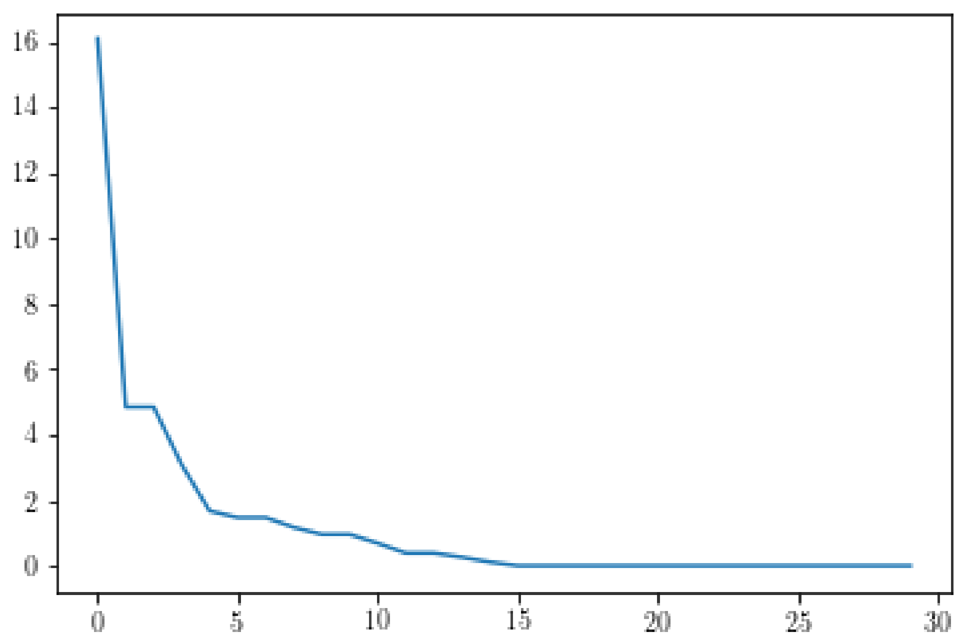
```
values = np.abs(values)

# finding eigenvectors corresponding to largest eval
lam = values[0]
lvec = left[:, 0]
rvec = right[:, 0]
```

In [546]:
```
values
```

Out[546]:
```
array([1.61091323e+01, 4.85096874e+00, 4.85096874e+00, 3.08542245e+00,
       1.67777730e+00, 1.47324012e+00, 1.47324012e+00, 1.17292964e+00,
       9.59011312e-01, 9.59011312e-01, 6.88101872e-01, 3.87433784e-01,
       3.87433784e-01, 2.60638428e-01, 1.11981802e-01, 3.59112222e-16,
       3.16622533e-16, 3.16622533e-16, 1.89127395e-16, 1.89127395e-16,
       1.39586372e-16, 9.76917161e-17, 1.00574144e-16, 7.59739866e-17,
       7.59739866e-17, 5.95954100e-17, 5.95954100e-17, 2.73320115e-17,
       2.73320115e-17, 3.05862567e-17])
```

In [547]:
```
plt.plot(values)
```

Out[547]:
```
[<matplotlib.lines.Line2D at 0x140c2bba470>]
```



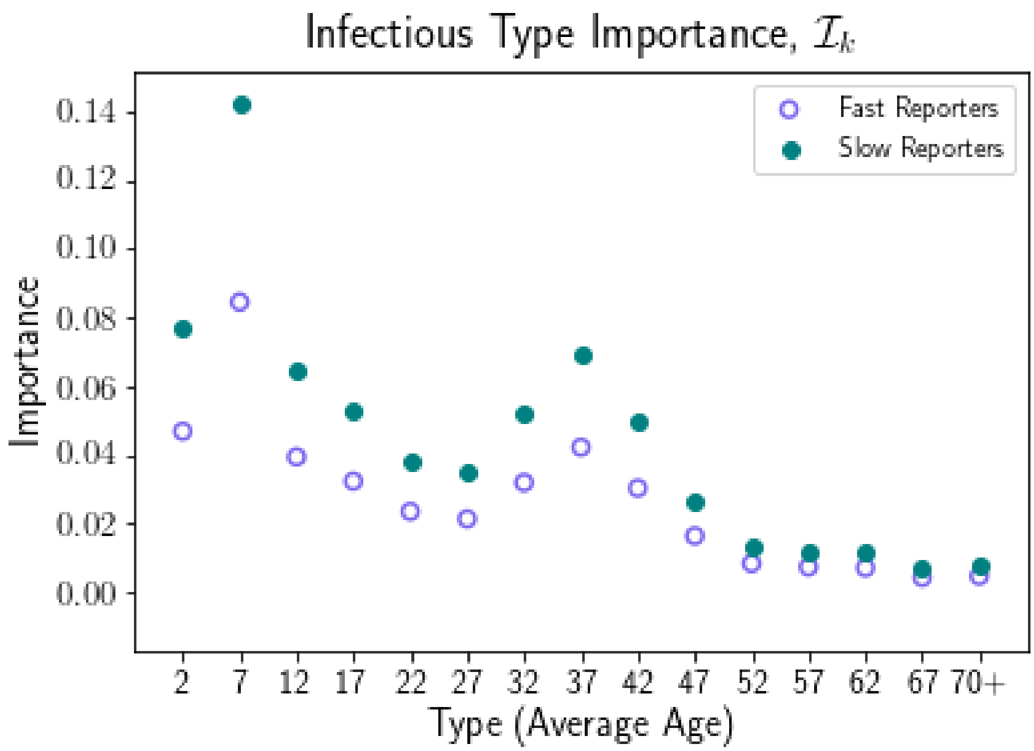
0.2.2 Type and Contact Importance

In [548]:
```
def type_importance(K, lam, lvec, rvec):
    arr = []
```

```
    norm = lvec.dot(rvec)
    for i in range(len(lvec)):
        arr.append((rvec[i]*lvec[i]) / (norm - lvec[i]*rvec[i]))
    return arr
```

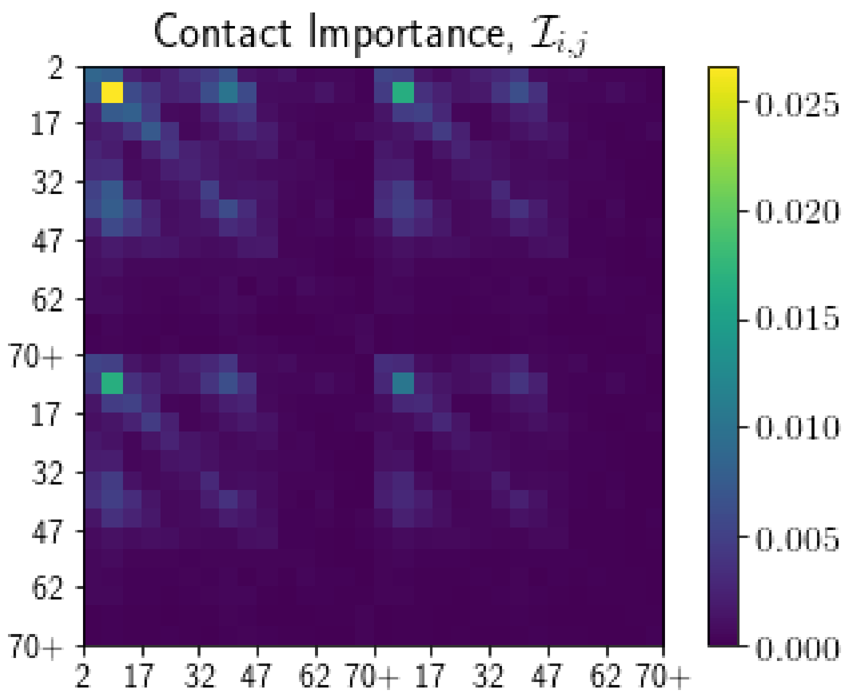
```
In [549]: I_type = type_importance(K, lam, lvec, rvec)
```

```
In [562]: plt.scatter(range(len(I_type))[:len(data)], I_type[len(data):], marker = "o", faceco
          plt.scatter(range(len(I_type))[:len(data)], I_type[:len(data)], color = "teal")
          plt.title("Infectious Type Importance, $\mathcal{I}_k$", fontsize = 17)
          plt.ylabel("Importance", fontsize  = 14)
          plt.xlabel("Type (Average Age)", fontsize = 14)
          plt.yticks(fontsize = 13)

          x = np.arange(0,15,1) # the grid to which your data corresponds
          nx = x.shape[0]
          no_labels = 9 # how many labels to see on axis x
          step_x = int(nx / (no_labels - 1)) # step between consecutive labels
          x_positions = np.arange(-0,nx - 0.5,step_x) # pixel count at label position
          x_labels = x[::step_x] # labels you want to see

          final_labels = []
          for idx in x_labels.astype(int):
              final_labels.append(age_range[idx])
          plt.xticks(x_positions, final_labels, fontsize = 12)

          plt.legend(["Fast Reporters", "Slow Reporters"])

          #plt.savefig("imgs/infectious_type.pdf", bbox_inches = "tight")
```




```
In [551]: age_range

Out[551]: [2, 7, 12, 17, 22, 27, 32, 37, 42, 47, 52, 57, 62, 67, '70+']

In [552]: def contact_importance(K, lam, lvec, rvec):
              norm = lvec.dot(rvec)
              I = np.zeros((len(K), len(K))) # K must be square matrix
              for i in range(len(I)):
                  for j in range(len(I)):
                      I[i,j] = K[i,j]*lvec[i]*rvec[j]/(lam * norm)

              return I

In [553]: I_contact = contact_importance(K, lam, lvec, rvec)

C:\Anaconda3\lib\site-packages\ipykernel_launcher.py:6: ComplexWarning: Casting complex values


In [564]: plt.imshow(I_contact)
          x = np.arange(0,31,1) # the grid to which your data corresponds
          nx = x.shape[0]
          no_labels = 10 # how many labels to see on axis x
          step_x = int(nx / (no_labels - 1)) # step between consecutive labels
```

```python
x_positions = np.arange(-0.5,nx -0.5,step_x) # pixel count at label position
x_labels = x[::step_x] # labels you want to see
x_labels = x_labels % 15
x_labels[5] = 15
x_labels[10] = 15

final_labels = []
for idk in x_labels:
    if idk == 15:
        final_labels.append(age_range[idk -1])
    else:
        final_labels.append(age_range[idk])

plt.xticks(x_positions, final_labels, fontsize = 12)
plt.yticks(x_positions, final_labels, fontsize = 12)

plt.title("Contact Importance, $\mathcal{I}_{i,j}$", fontsize = 17)
cbar = plt.colorbar()
cbar.ax.tick_params(labelsize=14)
#plt.savefig("imgs/contact_importance_png_version.png", dpi=600)
```

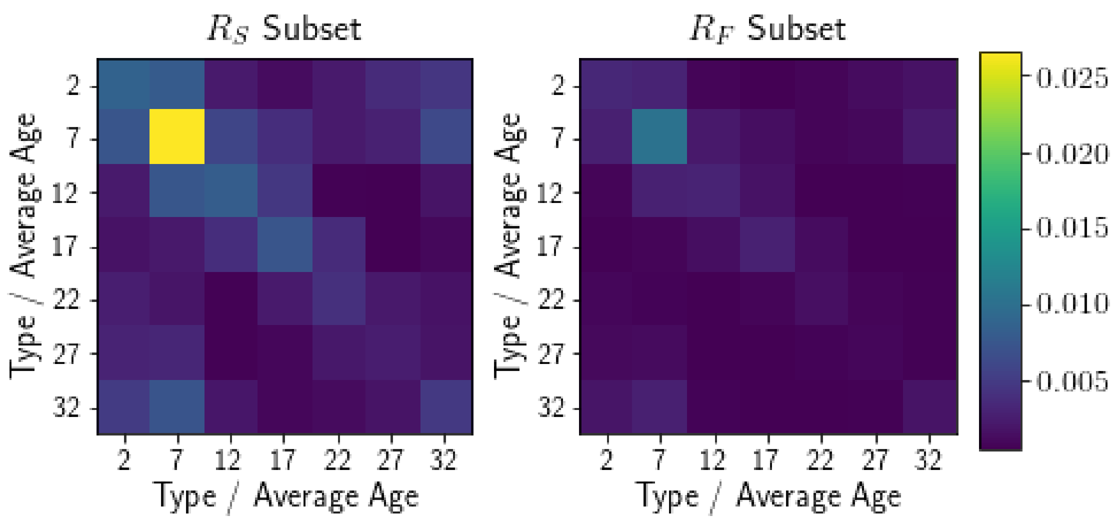



```python
In [555]: I_1 = I_contact[:7, :7]


          I_2 = I_contact[15:22, 15:22]
```

In [563]:
```
import matplotlib.colors as colors
import matplotlib
import copy


fig, (ax1, ax2) = plt.subplots(1,2)



colormap = matplotlib.cm.viridis #or any other colormap
normalize = matplotlib.colors.Normalize(vmin=np.min(I_1), vmax= np.max(I_1))
im1 = ax1.imshow(I_1, cmap=colormap, norm=normalize)


ax1.set_title("$R_S$ Subset", fontsize = 16)
ax1.set_xlabel("Type / Average Age", fontsize = 14)
ax1.set_ylabel("Type / Average Age", fontsize = 14)


ax2.imshow(I_2, cmap=colormap, norm=normalize)
ax2.set_title("$R_F$ Subset", fontsize = 16)
ax2.set_xlabel("Type / Average Age", fontsize = 14)
ax2.set_ylabel("Type / Average Age", fontsize = 14)


cbar_ax = fig.add_axes([1.0, 0.2, 0.04, 0.6])
cbar = plt.colorbar(im1, cax = cbar_ax)
cbar.ax.tick_params(labelsize=14)


final_labels = [2, 7, 12, 17, 22, 27, 32]
locs = ax1.get_yticks()


ax1.set_xticklabels( final_labels, fontsize = 12)

ax1.set_xticks(locs[1:-1])

ax1.set_yticklabels([""] + final_labels, fontsize = 12)

ax2.set_xticklabels( final_labels, fontsize = 12)

ax2.set_xticks(locs[1:-1])

ax2.set_yticklabels([""] + final_labels, fontsize = 12)

plt.tight_layout()
```

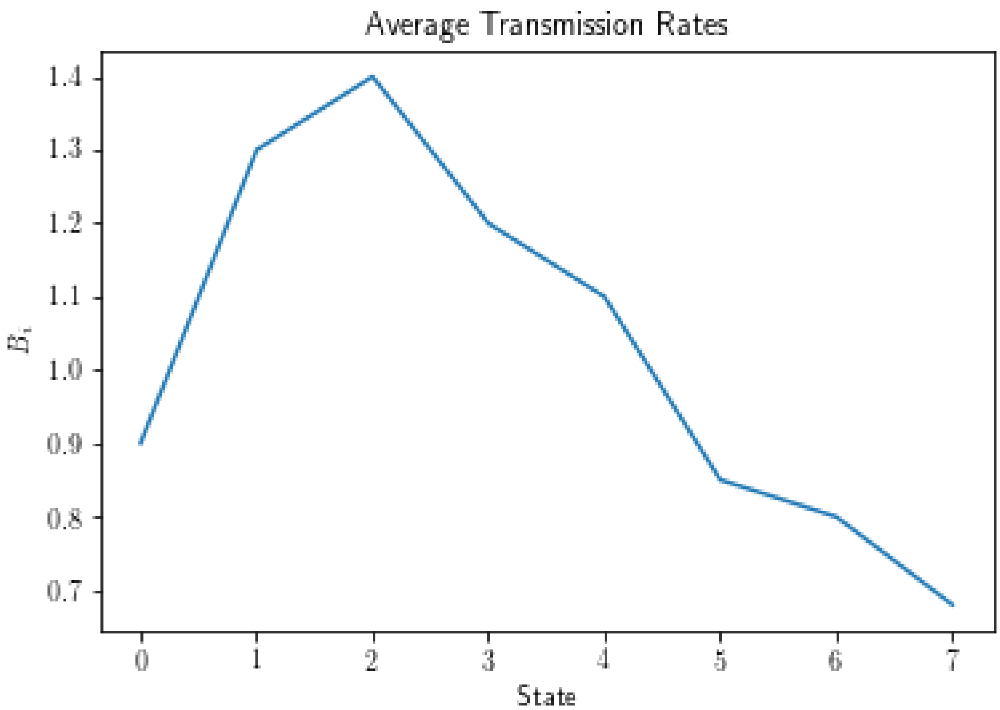
```
#plt.savefig("imgs/contact_importance_subset_plot.pdf", bbox_inches = "tight")
```

```
C:\Anaconda3\lib\site-packages\ipykernel_launcher.py:47: UserWarning: This figure includes Axe
```



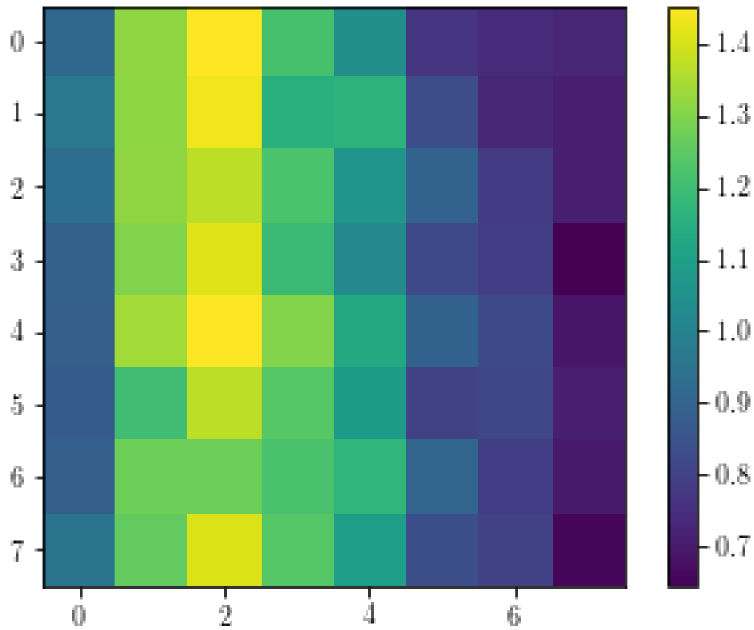
0.2.3 Second Example: Self-Generated Data

```
In [407]: # defining all parameters

          states = [0,1,2,3,4,5,6,7]
          average_transmission = [0.9, 1.3, 1.4, 1.2, 1.1, 0.85, 0.8, 0.68]
          mu = [1]*8
          Lambda = [1]*8
          Lambda[0] = 1.2
          gamma = 0.8 + 0.4*np.random.rand(8)

          # disease-free state values
          s_dfs = [0]*8
          for i in range(len(s_dfs)):
              s_dfs[i] = Lambda[i] / mu[i]


          plt.title("Average Transmission Rates")
          plt.ylabel("$B_i$")
          plt.xlabel("State")
          plt.plot(states, average_transmission)
          plt.show()
```



In [408]:
```
# generating the actual transmission rates
# sampling from a normal distribution w/ mean of the transmisson rates and a std of

B = np.zeros((8,8))
for i in range(8):
    mean = average_transmission[i]
    for j in range(8):
        B[j,i] = 0.05*np.random.randn() + mean
```

In [409]:
```
plt.imshow(B)
plt.colorbar()
plt.show()
```



0.2.4 Next Generation Matrix

We obtain the next generation matrix $\mathbf{G}$ by first constructing two matrices $\mathbf{T}$ and $\mathbf{\Sigma}$ so that

$$\dot{\mathbf{x}} = (\mathbf{T} + \mathbf{\Sigma})\mathbf{x}, \quad \text{where } \mathbf{x} = (I_1, I_2, ..., I_n)^T.$$

The matrix $\mathbf{T}$ represents terms in the ODE system that contribute to the disease transmission; in our example

$$\mathbf{T} = \begin{bmatrix} B_{11}S_1^* & B_{12}S_1^* & \dots & B_{1n}S_1^* \\ \vdots & \ddots & & \vdots \\ B_{n1}S_n^* & \dots & & B_{nn}S_n^* \end{bmatrix}.$$

Likewise, the matrix $\mathbf{\Sigma}$ represents all non-disease related transmissions within the infectious subsystem. In our example, this is

$$\mathbf{\Sigma} = \begin{bmatrix} -(\gamma_1 + \mu_1) & 0 & \dots & 0 \\ 0 & -(\gamma_2 + \mu_2) & \dots & 0 \\ \vdots & \ddots & & \vdots \\ 0 & \dots & & -(\gamma_n + \mu_n) \end{bmatrix}.$$

Using the fact that $\mathbf{G} = -\mathbf{T}\mathbf{\Sigma}^{-1}$, we have the next generation matrix:

$$\mathbf{G} = \begin{bmatrix} \frac{B_{11}S_1^*}{\gamma_1+\mu_1} & \frac{B_{12}S_1^*}{\gamma_2+\mu_2} & \dots & \frac{B_{1n}S_1^*}{\gamma_n+\mu_n} \\ \vdots & \ddots & & \vdots \\ \frac{B_{n1}S_n^*}{\gamma_1+\mu_1} & \dots & & \frac{B_{nn}S_n^*}{\gamma_n+\mu_n} \end{bmatrix}.$$

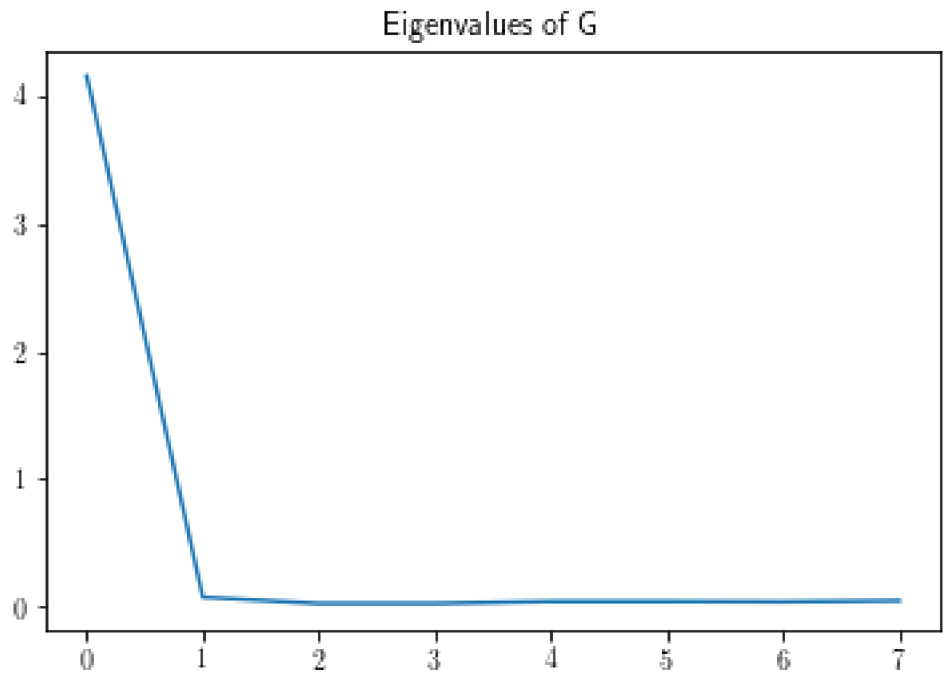
```python
In [410]: T = np.zeros((8,8))
          Sigma = np.zeros((8,8))

          for i in range(8):
              for j in range(8):
                  T[i,j] = B[i,j]*s_dfs[i]
                  if i ==j:
                      Sigma[i,j] = -(gamma[i] + mu[i])

          G = -T.dot(np.linalg.inv(Sigma))
```

0.2.5 Infective State Importance

By computing eigenvectors and the largest eigenvalue of **G**, we can find an approximation to the importance of each infectious state.

```python
In [411]: import scipy.linalg

          values, left, right = scipy.linalg.eig(G, right = True, left = True)

          values = np.abs(values)

In [412]: # l_e-  largest eigenvalue
          # lvec - corresponding left eigenvector
          # rvec - corresponding right eigenvector
          l_e = values[0]
          lvec = left[:, 0]
          rvec = right[:, 0]

          print("The Largest Eigenvalue of the Matrix is: " + str(np.round(l_e,2)))
          plt.plot(values)
          plt.title("Eigenvalues of G")
          plt.show()
```

```
The Largest Eigenvalue of the Matrix is: 4.16
```

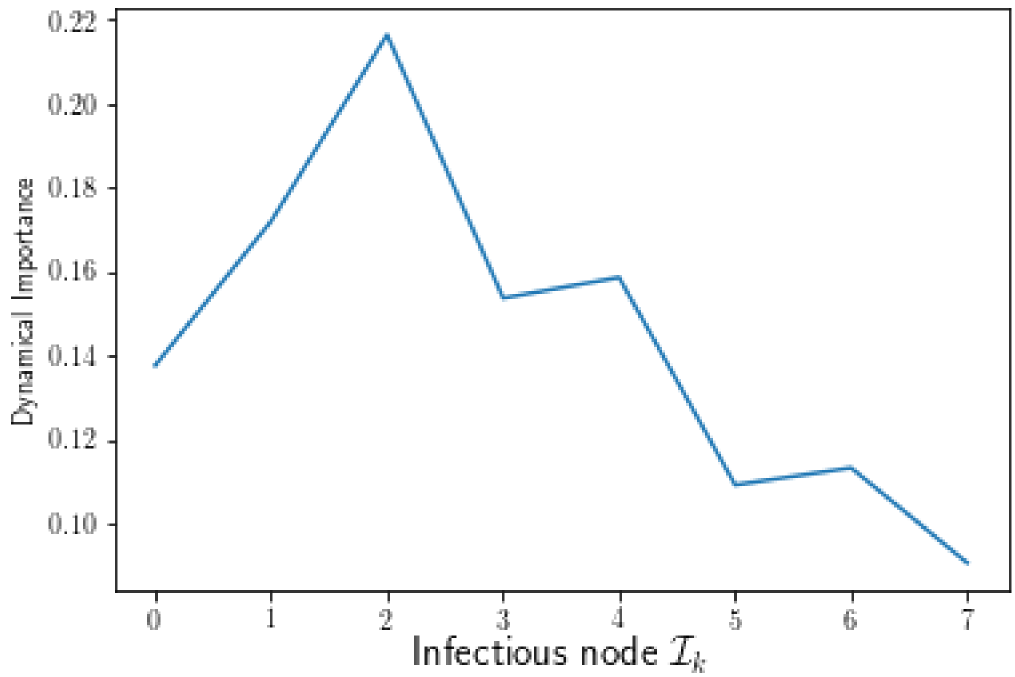



```
In [413]: # finding the important of each state from the eigenvalues and eigenvectors

          imp_list = []
          norm = abs(lvec.dot(rvec))
          print("Relative Importance of Infectious nodes for contribution to R_0:")
          for i in range(len(lvec)):
              imp = np.real(rvec[i]*lvec[i] / (norm - rvec[i]*lvec[i]))
              imp_list.append(imp)
              print("I_{}".format(i+1) + " = " + str(np.round(imp,2)))
```

```
Relative Importance of Infectious nodes for contribution to R_0:
I_1 = 0.14
I_2 = 0.17
I_3 = 0.22
I_4 = 0.15
I_5 = 0.16
I_6 = 0.11
I_7 = 0.11
I_8 = 0.09
```

```
In [414]: plt.plot(imp_list)
          plt.ylabel("Dynamical Importance")
          plt.xlabel("Infectious node $\mathcal{I}_k$", fontsize = 15)
          #plt.savefig("node_importance.pdf", bbox_inches = "tight")
```

Out[414]: Text(0.5, 0, 'Infectious node $\\mathcal{I}_k$')



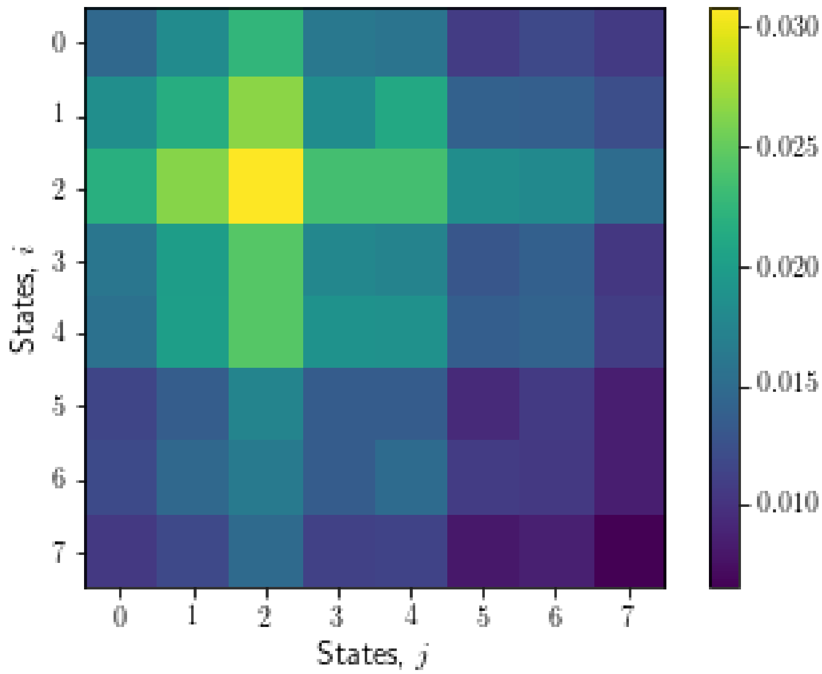
0.2.6 Importance Matrix of the Contacts between the members of the population

In [415]:
```
I = np.zeros((8,8))
for i in range(8):
    for j in range(8):
        I[i,j] = G[i,j]*lvec[i]*rvec[j] / (l_e*norm)
```

```
C:\Anaconda3\lib\site-packages\ipykernel_launcher.py:4: ComplexWarning: Casting complex values
  after removing the cwd from sys.path.
```

In [416]:
```
plt.imshow(I)
plt.colorbar()
plt.locator_params(axis='x', nbins=8)
plt.xlabel("States, $j$", fontsize = 12)
plt.ylabel("States, $i$", fontsize = 12)
#plt.savefig("edge_importance.pdf", bbox_inches = "tight")
```

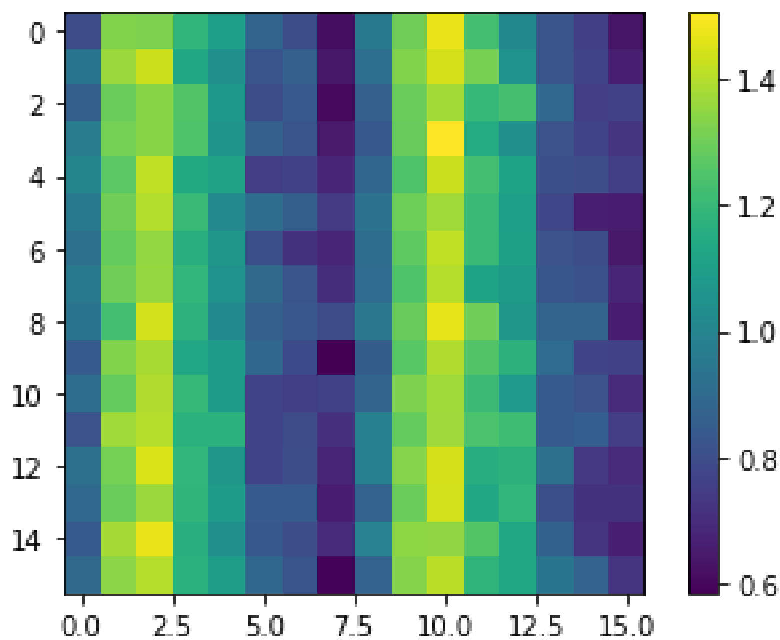
Out[416]: Text(0, 0.5, 'States, i')



0.2.7 Extension, Male and Female Seperation without a Contact Matrix

```
In [26]: # defining all parameters

         states = list(range(16))
         average_transmission = [0.9, 1.3, 1.4, 1.2, 1.1, 0.85, 0.8, 0.68]*2
         mu = [1]*16
         Lambda = [1]*16
         Lambda[0] = 1.2
         Lambda[8] = 1.2
         gamma_1 = 0.9 + 0.4*np.random.rand(8) # slow responders
         gamma_2 = 0.6 + 0.2*np.random.rand(8) # fast responders

         gamma = np.concatenate((gamma_1, gamma_2))
         # disease-free state values
         s_dfs = [0]*16
         for i in range(len(s_dfs)):
             s_dfs[i] = Lambda[i] / gamma[i]


         # plt.title("Average Transmission Rates")
         # plt.ylabel("B_i")
         # plt.xlabel("State")
         # plt.plot(states, average_transmission)
         # plt.show()
```

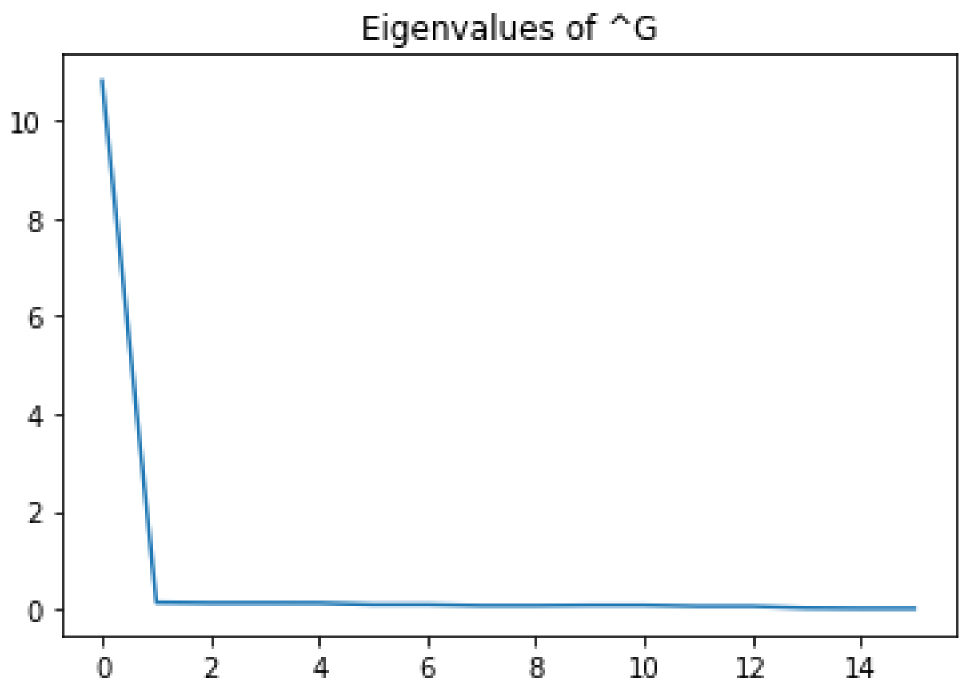
In [27]:
```
# generating the actual transmission rates
# sampling from a normal distribution w/ mean of the transmisson rates and a std of 0

B = np.zeros((16,16))
for i in range(16):
    mean = average_transmission[i]
    for j in range(16):
        B[j,i] = 0.05*np.random.randn() + mean

plt.imshow(B)
plt.colorbar()
plt.show()
```



In [28]:
```
# Generating the Next Generation Matrix

T = np.zeros((16,16))
Sigma = np.zeros((16,16))

for i in range(16):
    for j in range(16):
        T[i,j] = B[i,j]*s_dfs[i]
        if i ==j:
            Sigma[i,j] = -(gamma[i] + mu[i])

G = -T.dot(np.linalg.inv(Sigma))
```

In [29]:
```
import scipy.linalg

values, left, right = scipy.linalg.eig(G, right = True, left = True)
values = np.abs(values)

# l_e-  largest eigenvalue
# lvec - corresponding left eigenvector
# rvec - corresponding right eigenvector
l_e = values[0]
lvec = left[:, 0]
rvec = right[:, 0]

print("The Largest Eigenvalue of the Matrix is: " + str(np.round(l_e,2)))
plt.plot(values)
plt.title("Eigenvalues of ^G")
plt.show()
```

```
The Largest Eigenvalue of the Matrix is: 10.82
```



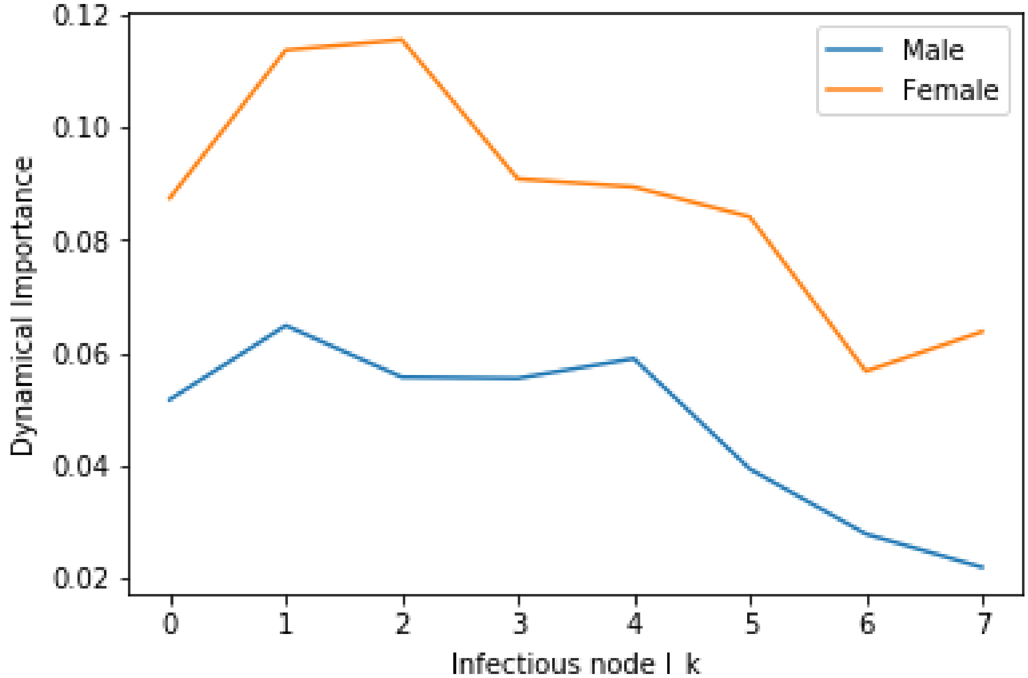
In [30]:
```
# finding the important of each state from the eigenvalues and eigenvectors

imp_list = []
norm = abs(lvec.dot(rvec))
print("Relative Importance of Infectious nodes for contribution to R_0:")
```

```
for i in range(len(lvec)):
    imp = np.real(rvec[i]*lvec[i] / (norm - rvec[i]*lvec[i]))
    imp_list.append(imp)
    print("I_{}".format(i+1) + " = " + str(np.round(imp,2)))
```

```
Relative Importance of Infectious nodes for contribution to R_0:
I_1 = 0.05
I_2 = 0.06
I_3 = 0.06
I_4 = 0.06
I_5 = 0.06
I_6 = 0.04
I_7 = 0.03
I_8 = 0.02
I_9 = 0.09
I_10 = 0.11
I_11 = 0.12
I_12 = 0.09
I_13 = 0.09
I_14 = 0.08
I_15 = 0.06
I_16 = 0.06
```

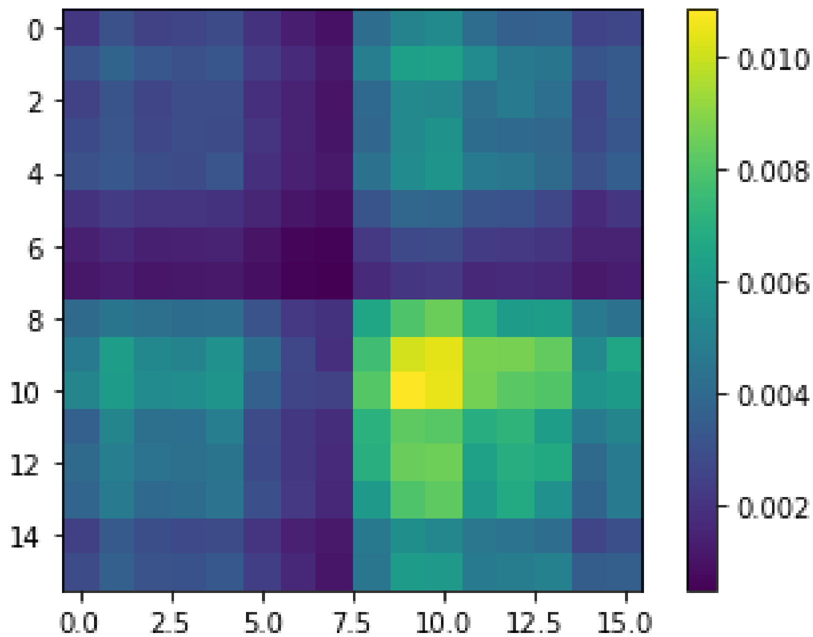
```
In [31]: plt.plot(imp_list[:8])
         plt.ylabel("Dynamical Importance")
         plt.xlabel("Infectious node I_k")
         plt.plot(imp_list[8:])
         plt.legend(["Male", "Female"])
```

```
Out[31]: <matplotlib.legend.Legend at 0x1531c358da0>
```




```
In [32]: I = np.zeros((16,16))
         for i in range(16):
             for j in range(16):
                 I[i,j] = G[i,j]*lvec[i]*rvec[j] / (l_e*norm)

         plt.imshow(I)
         plt.colorbar()
         plt.show()
```

```
C:\Anaconda3\lib\site-packages\ipykernel_launcher.py:4: ComplexWarning: Casting complex values
  after removing the cwd from sys.path.
```




```
In [ ]:
```